We Claim:

1. A method of karyotyping a genome of a test eukaryotic cell, comprising:

generating a population of sequence tags from defined portions of the genome of the test eukaryotic cell, said portions being defined by one or two restriction endonuclease recognition sites;

enumerating said sequence tags in the population to determine the number of individual sequence tags present in the population;

comparing the number of a plurality of sequence tags in the population to the number of the plurality of sequence tags determined for a genome of a reference cell, wherein the plurality of sequence tags are within a window of sequence tags which are calculated to be contiguous in the genome of the species of the eukaryotic cell, wherein a difference in the number of the plurality of sequence tags within the window present in the population from the number determined for a reference eukaryotic cell indicates a karyotypic difference between the test eukaryotic cell and the reference eukaryotic cell.

2. The method of claim 1 wherein the test eukaryotic cell and the reference eukaryotic cell are of the same species.
3. The method of claim 1 wherein the plurality of sequence tags comprises 10 to 500 contiguous sequence tags.
4. The method of claim 1 wherein the plurality of sequence tags comprises 50 to 1000 contiguous sequence tags.
5. The method of claim 1 wherein the test eukaryotic cell is a human cell.
6. The method of claim 1 wherein the window spans about 40 kb.
7. The method of claim 1 wherein the window spans about 200 kb.
8. The method of claim 1 wherein the window spans about 600 kb.
9. The method of claim 1 wherein the window spans about 4 Mb.
10. The method of claim 1 wherein less than 50 % of the sequence tags calculated to be present in the genome of the eukaryotic cell are enumerated in the step of enumerating.

11. The method of claim 1 wherein less than 33 % of the sequence tags calculated to be present in the genome of the eukaryotic cell are enumerated in the step of enumerating.
12. The method of claim 1 wherein less than 25 % of the sequence tags calculated to be present in the genome of the eukaryotic cell are enumerated in the step of enumerating.
13. The method of claim 1 wherein less than 20 % of the sequence tags calculated to be present in the genome of the eukaryotic cell are enumerated in the step of enumerating.
14. The method of claim 1 wherein less than 15 % of the sequence tags calculated to be present in the genome of the eukaryotic cell are enumerated in the step of enumerating.
15. The method of claim 1 wherein the test eukaryotic cell is a cancer cell.
16. The method of claim 1 wherein the test eukaryotic cell is a cell of a person with a hereditary disorder.
17. The method of claim 1 wherein the test eukaryotic cell is a cell of a person with an infectious disease.
18. The method of claim 1 wherein said portions are defined by a first restriction endonuclease cleavage site at a first end of each portion and a second restriction endonuclease cleavage site at a second end of each portion.
19. The method of claim 18 wherein the first restriction endonuclease is SacI.
20. The method of claim 18 wherein the second restriction endonuclease is NlaIII.
21. The method of claim 18 wherein recognition or cleavage by the first restriction endonuclease is sensitive to DNA methylation.
22. The method of claim 1 wherein said portions are defined by presence of a BcgI restriction endonuclease recognition site which is flanked by 12 nucleotides on either end.
23. The method of claim 1 further comprising:
identifying aneuploidy if (a) sequence tags of one or more autosomes are determined to be present in the test eukaryotic cell relative to the reference eukaryotic cell at a

ratio of 1.5 or greater or less than 0.7; or (b) sequence tags of one or more sex chromosomes in a male are determined to be present in the test eukaryotic cell relative to a reference male eukaryotic cell at a ratio of 1.5 or greater or less than 0.7; or (c) sequence tags of X chromosomes in a female are determined to be present in the test eukaryotic cell relative to a reference male eukaryotic cell at a ratio of 3 or greater or less than 1.5 or relative to a reference female eukaryotic cell at a ratio of 1.5 or greater or less than 0.7.

24. The method of claim 1 wherein the step of enumerating is performed by determining the nucleotide sequence of said sequence tags and recording the number of occurrences of individual sequence tags.
25. A dimer comprising two distinct sequence tags from defined portions of a genome of a eukaryotic cell, said portions being defined by one or two restriction endonuclease recognition sites, wherein each of said sequence tags consists of a fixed number of nucleotides of one of said defined portions of the genome, said fixed number of nucleotides extending from at least one of said restriction endonuclease recognition sites.
26. The dimer of claim 25 wherein said portions are defined by a first restriction endonuclease site at a first end of each portion and a second restriction endonuclease site at a second end of each portion.
27. The dimer of claim 26 wherein the two sequence tags are joined end-to-end at the ends distal to the second restriction endonuclease site.
28. The dimer of claim 26 further comprising a linker oligonucleotide ligated at each second restriction endonuclease site of the two sequence tags.
29. The dimer of claim 25 wherein the eukaryotic cell is a human cell.
30. A concatamer of dimers according to claim 25.
31. A concatamer of dimers according to claim 26.
32. A concatamer of dimers according to claim 27.
33. A concatamer of dimers according to claim 28.

34. The dimer of claim 25 wherein the fixed number of nucleotides is determined by a Type IIS restriction endonuclease used to cleave within said defined portions of the genome.

35. The dimer of claim 34 wherein the Type IIS restriction endonuclease is *Mme*I.

36. The dimer of claim 35 wherein the fixed number of nucleotides is 20 to 22.

37. A method of karyotyping a genome of a test eukaryotic cell, comprising:

generating a population of sequence tags from defined portions of the genome of the test eukaryotic cell, said portions being defined by one or two restriction endonuclease recognition sites;

enumerating said sequence tags in the population to determine the number of individual sequence tags present in the population;

comparing the number of a plurality of sequence tags in the population to the number of said plurality of sequence tags calculated to be present in the human genome, wherein the plurality of sequence tags are within a window of sequence tags which are calculated to be contiguous in the genome of the species of the eukaryotic cell, wherein a difference in the number of the plurality of sequence tags within the window present in the population from the number calculated to be present in the genome of the eukaryotic cell indicates a karyotypic abnormality.

38. The method of claim 37 wherein said portions are defined by a first restriction endonuclease site at a first end of each portion and a second restriction endonuclease site at a second end of each portion.

39. The method of claim 37 wherein said portions are defined by presence of a *Bcg*I restriction endonuclease recognition site which is flanked by 12 nucleotides on either end.

40. The method of claim 37 wherein the window comprises 10 to 500 contiguous tags.

41. The method of claim 37 wherein the window comprises 50 to 1000 contiguous tags.

42. The method of claim 37 wherein the test eukaryotic cell is a human cell.

43. The method of claim 37 wherein the window spans about 40 kb.

44. The method of claim 37 wherein the window spans about 200 kb.

45. The method of claim 37 wherein the window spans about 600 kb.

46. The method of claim 37 wherein the window spans about 4 Mb.
47. The method of claim 37 wherein less than 50 % of the sequence tags calculated to be present in the genome of the eukaryotic cell are enumerated in the step of enumerating.
48. The method of claim 37 wherein less than 33 % of the sequence tags calculated to be present in the genome of the eukaryotic cell are enumerated in the step of enumerating.
49. The method of claim 37 wherein less than 25 % of the sequence tags calculated to be present in the genome of the eukaryotic cell are enumerated in the step of enumerating.
50. The method of claim 37 wherein less than 20 % of the sequence tags calculated to be present in the genome of the eukaryotic cell are enumerated in the step of enumerating.
51. The method of claim 37 wherein less than 15 % of the sequence tags calculated to be present in the genome of the eukaryotic cell are enumerated in the step of enumerating.
52. The method of claim 37 wherein the test eukaryotic cell is a cancer cell.
53. The method of claim 37 wherein the test eukaryotic cell is a cell of a person with a hereditary disorder.
54. The method of claim 37 wherein the cell is a cell of a person with an infectious disease.
55. The method of claim 38 wherein the first restriction endonuclease is *Sac*I.
56. The method of claim 38 wherein the second restriction endonuclease is *Nla*III.
57. The method of claim 38 wherein recognition or cleavage by the first restriction endonuclease is sensitive to DNA methylation.
58. The method of claim 37 wherein the step of enumerating is performed by determining the nucleotide sequence of said sequence tags and recording the number of occurrences of individual sequence tags.